

SEQUENCE LISTING

<110> Ruben et al.

<120> Human Tumor Necrosis Factor Receptor TR17

<130> PF524P1

<140> Unassigned

<141> 2001-09-25

<150> 60/254,874

<151> 2000-12-13

<150> 60/235,991

<151> 2000-09-26

<150> 09/533,822

<151> 2000-03-24

<150> 60/188,208

<151> 2000-03-10

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 882

<212> DNA

<213> Homo sapiens

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<222> (1)..(882)

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cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg gtg gct atg aga 96  
Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg  
20 25 30

tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg ggt acc tgc atg 144  
Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met  
35 40 45

tcc tgc aaa acc att tgc aac cat cag agc cag cgc acc tgt gca gcc 192  
Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala  
50 55 60

ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc aag ttc tat gac 240  
Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp  
65 70 75 80

cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt gga cag cac 288  
His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His  
85 90 95

cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg agc cca gtg Pro Lys Cln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val 100 105 110	336
aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa gtt gaa aac Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn 115 120 125	384
aat tca gac aac tcg gga agg tac caa gga ttg gag cac aga ggc tca Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser 130 135 140	432
gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca gat cag gtg Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val 145 150 155 160	480
gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt gcc gtc ctc tgc Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys 165 170 175	528
tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag agg ggg gat ccc Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro 180 185 190	576
tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt ccg gcc aag tct Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser 195 200 205	624
tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg agc aca tcc ccc Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro 210 215 220	672
gag cca gtg gag acc tgc agc ttc tgc ttc cct gag tgc agg gcg ccc Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro 225 230 235 240	720
acg cag gag agc gca gtc acg cct ggg acc ccc gac ccc act tgt gct Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala 245 250 255	768
gga agg tgg ggg tgc cac acc agg acc aca gtc ctg cag cct tgc cca Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro 260 265 270	816
cac atc cca gac agt ggc ctt ggc att gtg tgt gtg cct gcc cag gag His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu 275 280 285	864
ggg ggc cca ggt gca taa Gly Gly Pro Gly Ala 290	882

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 35 40 45  
 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala  
 50 55 60  
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp  
 65 70 75 80  
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His  
 85 90 95  
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val  
 100 105 110  
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn  
 115 120 125  
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser  
 130 135 140  
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val  
 145 150 155 160  
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys  
 165 170 175  
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro  
 180 185 190  
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser  
 195 200 205  
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro  
 210 215 220  
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro  
 225 230 235 240  
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala  
 245 250 255  
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro  
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 tctccggac tcctgaggtc acatgcgtgg tggtgacgt aagccacgaa gaccctgagg 180  
 tcaagtcaa ctggtagctg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240  
 aggagcagta caacagcagc taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300  
 ggctgaatgg caaggagttac aagtgcagg tctccaacaa agccctccca acccccatcg 360  
 agaaaaaccat ctccaaagcc aaaggccagc cccgagaacc acaggtgtac accctgccc 420  
 catccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggc aaaggcttct 480  
 atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540  
 ccacgcctcc cgtgctggac tccgacggct cttcttcct ctacagcaag ctcaccgtgg 600  
 acaagagcag gtggcagcag gggAACgtct tctcatgctc cgtgatgcat gaggctctgc 660  
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Ala

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Trp Ala Pro Ala Arg Gly  
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